IN THE SPECIFICATION:

Please replace the paragraph appearing in the as-filed specification at page 18, line 21 to page 19, line 2 (paragraph **[0057]** of the substitute specification filed March 18, 2002), with the following replacement paragraph:

[0057] In FIG. 2, Primer 6AR-1 could not be extended with template HCV genotype 1a when using either dCTP plus dTTP, or dCTP plus dGTP as substrates due to a CA deletion (..), resulting either in a mispair at nucleotide position -145 in front of the 3' end of primer (FIG. ~~1~~2, column I-1) or in only one matched pairing at the position (FIG. ~~1~~2, column I-2). Primer 6AR-1 could not be extended on template HCV genotype 6a when using dCTP and dGTP (FIG. ~~1~~2, column I-3). However, the primer was extended by three bases with template HCV genotype 6a using dGTP and dTTP which matched the nucleotides in the CA insertion (CA) in template HCV genotype 6a (FIG. ~~1~~2, column I-4). Primer 6AR-2 was extended when using template HCV genotype 6a (FIG. ~~1~~2, column II-1 and column II-2), but not with template HCV genotype 1a using either dATP, dCTP and dGTP or only dGTP (FIG. ~~1~~2, column II-3 and column II-4). The symbol ↔ denotes the removal of the first nucleotide mismatched at the 3' end of the primer.

Please replace the paragraph appearing in the as-filed specification at page 19, line 30 to page 20, line 12 (paragraph **[0060]** of the substitute specification filed March 18, 2002), with the following replacement paragraph:

[0060] Like mispair formation and extension by T4 DNA polymerase (Wilber, J. C., *et al.*, M. S. Reverse transcriptase-PCR for hepatitis C virus RNA, p. 327-331. *In* D. H. Persing, T.F. Smith, F.C. Tenover, and T.J. White (ed.), Diagnostic Molecular Microbiology: Principles and Applications. American Society for Microbiology, Washington D.C. 1993), any two or more consecutive mispairs could completely terminate primer extension by *pfu* because of its 3'→5' proofreading activity (FIG. 1, column II-2 and FIG. 2, I-3 and II-2). It was also found that two or more mispairs, separated by one or two correct base pairs (FIG. 1, column II-1 and FIG. 2, II-1) could also terminate primer extension by *pfu*. Use of the termination point caused by these mispairs as well as primer specific and mispair extensions as shown in FIG. 1, columns II-1, II-2 and II-3 on templates by *pfu* provided reliable information on nucleotide sequence in the given region of the 5' UR of HCV.